

### **REMARKS**

Applicants have amended claims 32 and 39 to include embodiments for identifying single nucleotide polymorphisms (SNPs) in the genome of mammals of the same species. These embodiments derive from Applicants' discovery of the distribution and density of SNPs in a mammalian genome and their penetrating insight that combining SNPs would provide valuable genetic information. Applicants, in their specification, teach and enable the advantageous properties of SNPs for genetic analysis in, among other things, mammals. See the specification, for example, at pages 13-15, page 44, lines 29-36 and Examples 1-6. Moreover, Applicants teach and enable using the combinations of SNPs, even at high allelic frequencies, to provide highly accurate genetic analysis. See the specification, for example, at pages 38-42, Examples 1-6 and Figures 4 and 5.

Applicants have also added new claims 56-58, which include parentage testing that the Examiner implicitly suggests meets the written description requirement. (See Final Office Action, Item 12) Support for new claims 56-58 can be found, for example, at page 37, lines 18-25, pages 41-43 and 47, original claim 12, and Examples 1, 2 and 4. No new matter has been added. Applicants respectfully request entry of this amendment and reconsideration of the application.

### **Objection to the Specification**

The Examiner has objected to the specification for failing to indicate the status of certain applications and for certain documents improperly incorporated by reference into the specification. Applicants respectfully disagree with the Examiner's position. Nevertheless, Applicants have amended the specification to include the status of the application and remove the alleged improper incorporation by reference of certain documents. Applicants respectfully submit that the Examiner's objection is moot in light of the amendments to the specification.

**Rejection under 35 U.S.C. §112, First Paragraph: Written Description**

The Examiner rejected claims 32-45 under 35 U.S.C. §112, first paragraph for allegedly failing to comply with the written description requirement. Applicants respectfully traverse this rejection.

The Examiner asserts that the specification does not provide adequate written description for identifying single nucleotide polymorphisms in myriad of "species of interests", which includes all life forms including viruses. The Examiner acknowledges that the specification does provide several examples directed to equine and horse DNA. However, the Examiner concludes that there is no written description for the myriad of claimed species of interest.

Applicants respectfully disagree with this rejection, but have amended claims 32-45 in order to expedite prosecution to include methods for identifying single nucleotide polymorphic sites in the genome of mammals of **the same species**.

Applicants submit the specification provides written description and fully enables the claims. The specification at pages 13-15, page 44, lines 29-36 and Examples 1-6 clearly discloses and enables conducting genetic analysis using SNPs from mammalian DNA. Applicants submit that genomic DNA is genomic DNA regardless of the species. Thus, DNA does not chemically vary between species and the analysis of SNPs should not in any way depend on the source of the nucleic acid molecules.

To provide further support, Applicants performed a limited sequence search for mammals other than horses using NIH BLAST search for exact matches of some of the sequences described in Table I of the specification: Sequences ID Nos. 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 25, 45, and 71. Exact matches were found for mammals other than horses, for example in humans, chimpanzees, mice, rat, cow, ring-tailed lemurs and opossums. The BLAST results are listed below.

SEQ ID NO	BLAST MATCH	SPECIES
1 (C Allele)	gi 19852154 gb AC023315.4  Homo sapiens chromosome 17, clone RP11-333J10, complete sequence Length = 135692 Score = 34.2 bits (17), Expect = 2.1 Identities = 17/17 (100%) Strand = Plus / Minus  Query: 5 ctctaagtgtgtgggc 21         Sbjct:117900 ctctaagtgtgtgggc 117884	Human
1 (T Allele)	gi 31194043 gb AC129322.3  Mus musculus BAC clone RP23-220F4 from chromosome 19, complete sequence Length = 182093 Score = 32.2 bits (16), Expect = 8.3 Identities = 19/20 (95%) Strand = Plus / Minus  Query: 2 cagctctaagtgtgtgggt 21         Sbjct: 88019 cagctctaagtcagtggt 88000	House Mouse
1 (T Allele)	gi 25815276 gb AC069513.28  Homo sapiens 3 BAC RP11-171N2 (Roswell Park Cancer Institute Human BAC Library) complete sequence Length = 174097 Score = 32.2 bits (16), Expect = 8.3 Identities = 16/16 (100%) Strand = Plus / Minus  Query: 6 tctaagtgtgtgggt 21         Sbjct: 22999 tctaagtgtgtgggt 22984	Human
3 (G Allele)	gi 39725895 gb AC147117.2  Pan troglodytes BAC clone CH251-532B3 from Y, complete sequence Length = 207020 Score = 34.2 bits (17), Expect = 2.1 Identities = 17/17 (100%) Strand = Plus / Plus  Query: 5 ccttagaatttctgcag 21         Sbjct: 58093 ccttagaatttctgcag 58109	Chimpanzee

<p>3 (G Allele)</p>	<p>gi 56236323 gb AC145551.5  Mus musculus chromosome UNKNOWN clone RP23-73014, complete sequence  Length = 204610    Score = 34.2 bits (17), Expect = 2.1  Identities = 17/17 (100%)  Strand = Plus / Plus    Query: 5 ccttagaatttctgcag 21         Sbjct: 77512 ccttagaatttctgcag 77528</p>	<p>Mouse</p>
<p>3 (G Allele)</p>	<p>gi 11322840 emb AL359641.10  Human DNA sequence from clone RP11-402K9 on chromosome Xq21.32-22.2  Contains a novel pseudogene and a laminin receptor 1 (ribosomal protein SA,67kDa) (LAMR1) pseudogene, complete sequence  Length = 175132    Score = 34.2 bits (17), Expect = 2.1  Identities = 17/17 (100%)  Strand = Plus / Plus    Query: 5 ccttagaatttctgcag 21         Sbjct: 86069 ccttagaatttctgcag 86085</p>	<p>Human</p>
<p>3 (A Allele)</p>	<p>gi 38044276 gb AC146159.2  Pan troglodytes BAC clone RP43-36019 from 7, complete sequence  Length = 163991  Score = 34.2 bits (17), Expect = 2.1  Identities = 17/17 (100%)  Strand = Plus / Minus    Query: 5 ccttagaatttctgcaa 21         Sbjct: 49782 ccttagaatttctgcaa 49766</p>	<p>Chimpanzee</p>
<p>3 (A Allele)</p>	<p>gi 5540113 gb AC008080.1 AC008080 Homo sapiens clone RP11-89N17 from 7p14-15, complete sequence  Length = 178635  Score = 34.2 bits (17), Expect = 2.1  Identities = 17/17 (100%)  Strand = Plus / Minus    Query: 5 ccttagaatttctgcaa 21         Sbjct: 53541 ccttagaatttctgcaa 53525</p>	<p>Human</p>

<p><b>3</b> (A Allele)</p>	<p>gi 58801546 ref NM_001003166.1  Canis familiaris CE8 protein, variant 2 (CE8), mRNA  Length = 789  Score = 34.2 bits (17), Expect = 2.1  Identities = 17/17 (100%)  Strand = Plus / Plus</p> <p>Query: 5 ccttagaatttctgcaa 21         Sbjct: 397 ccttagaatttctgcaa 413</p>	<p>Human</p>
<p><b>3</b> (A Allele)</p>	<p>gi 59709517 gb AC112984.21  Mus musculus chromosome 18, clone RP24-185P1, complete sequence  Length = 171822  Score = 32.2 bits (16), Expect = 8.3  Identities = 16/16 (100%)  Strand = Plus / Plus</p> <p>Query: 6 cttagaatttctgcaa 21         Sbjct: 93726 cttagaatttctgcaa 93741</p>	<p>House Mouse</p>
<p><b>5</b> (A Allele)</p>	<p>gi 29294367 gb AC130203.4  Mus musculus BAC clone RP24-413E20 from chromosome 15, complete sequence  Length = 182040  Score = 34.2 bits (17), Expect = 2.1  Identities = 17/17 (100%)  Strand = Plus / Minus</p> <p>Query: 1 agctctgggatgatcca 17         Sbjct: 79633 agctctgggatgatcca 79617</p>	<p>House Mouse</p>
<p><b>5</b> (A Allele)</p>	<p>gi 62000729 gb AC153981.5  Mus musculus 10 BAC RP24-112H16 (Roswell Park Cancer Institute (C57BL/6J Male) Mouse BAC Library) complete sequence  Length = 177129  Score = 34.2 bits (17), Expect = 2.1  Identities = 17/17 (100%)  Strand = Plus / Minus</p> <p>Query: 5 ctgggatgatccactaa 21         Sbjct: 166294 ctgggatgatccactaa 166278</p>	<p>House Mouse</p>
<p><b>5</b></p>	<p>gi 21217841 emb AL691483.10  Human DNA</p>	<p>Human</p>

(A Allele)	sequence from clone RP11-484M14 on chromosome 1, complete sequence Length = 90642 Score = 32.2 bits (16), Expect = 8.3 Identities = 16/16 (100%) Strand = Plus / Plus  Query: 6            tgggatgatccactaa 21       Sbjct: 32700       tgggatgatccactaa 32715	
7 (T Allele)	gi 21844648 gb AC115305.4  Mus musculus BAC clone RP24-372L1 from 18, complete sequence Length = 155389 Score = 34.2 bits (17), Expect = 2.1 Identities = 17/17 (100%) Strand = Plus / Plus  Query: 5            catcatttttcctcat 21       Sbjct: 142213       catcatttttcctcat 142229	House Mouse
7 (T Allele)	gi 22138730 emb AL590556.20  Human DNA sequence from clone RP11-26H16 on chromosome 1 Contains a ribosomal protein L21 (RPL21) pseudogene, the 5' end of the HSPG2 gene for heparan sulfate proteoglycan 2 (perlecan), the ELA3B gene for elastase 3B (pancreatic) and the ELA3A gene for elastase 3A (pancreatic (protease E)), complete sequence Length = 118495  Score = 34.2 bits (17), Expect = 2.1 Identities = 17/17 (100%) Strand = Plus / Minus  Query: 5            catcatttttcctcat 21       Sbjct: 93452       catcatttttcctcat 93436	Human
7 (C Allele)	gi 23462914 gb AC123044.4  Mus musculus BAC clone RP24-548B7 from chromosome 5, complete sequence Length = 184772 Score = 32.2 bits (16), Expect = 8.3 Identities = 16/16 (100%) Strand = Plus / Plus	House Mouse

	<p>Query: 6           atcattttttccctcac 21       </p> <p>Sbjct: 24180   atcattttttccctcac 24195</p>	
7 (C Allele)	<p><u>gi 23462914 gb AC123044.4 </u> Mus musculus  BAC clone RP24-548B7 from chromosome 5,  complete sequence  Length = 184772  Score = 32.2 bits (16), Expect = 8.3  Identities = 16/16 (100%)  Strand = Plus / Plus</p> <p>Query: 6           atcattttttccctcac 21       </p> <p>Sbjct: 24180   atcattttttccctcac 24195</p>	House Mouse
7 (C Allele)	<p><u>gi 18857856 emb Z98744.2 HS193B12</u> Human  DNA sequence from clone RP1-193B12 on  chromosome 6p21.3-22.3  Contains the H2AFD, H2BFD, H2AFI, H1F5,  H3FF, H4FK, H3FJ,  H2AFN, and H2BFN histone genes, the OR2B2  gene for olfactory receptor 2B2, histone  H2B family member I  pseudogene H2BFIP, a hypothetical protein  pseudogene,  ESTs, STSs, GSSs and CpG islands, complete  sequence  Length = 100374  Score = 34.2 bits (17), Expect = 2.1  Identities = 17/17 (100%)  Strand = Plus / Plus</p> <p>Query: 5           catcattttttccctcac 21       </p> <p>Sbjct: 11160   catcattttttccctcac 11176</p>	Human
9 (G Allele)	<p><u>gi 21738604 emb AL731817.11 </u> Mouse DNA  sequence from clone RP23-3J16 on  chromosome 11 Contains a  novel gene and the 3' end of a novel gene,  complete  sequence  Length = 103582  Score = 38.2 bits (19), Expect = 0.14  Identities = 19/19 (100%)  Strand = Plus / Minus</p> <p>Query: 3           aactaatttgatggccatg 21       </p> <p>Sbjct: 6142   aactaatttgatggccatg 6124</p>	House Mouse

<p>9 (A Allele)</p>	<p>gi 28971516 emb AL929426.8  Mouse DNA  sequence from clone RP23-471H23 on  chromosome 11 Contains  the 3' end of the Scep1 gene for serine  carboxypeptidase  1, complete sequence  Length = 52369</p> <p>Score = 34.2 bits (17), Expect = 2.1  Identities = 17/17 (100%)  Strand = Plus / Minus</p> <p>Query: 5            ctaatttgatggccata 21                            </p> <p>Sbjct: 1959        ctaatttgatggccata 1943</p>	<p>House Mouse</p>
<p>9 (A Allele)</p>	<p>gi 28564367 emb AL954650.8  Human DNA  sequence from clone RP11-523M19 on  chromosome 1, complete  sequence  Length = 86257  Score = 32.2 bits (16), Expect = 8.3  Identities = 16/16 (100%)  Strand = Plus / Minus</p> <p>Query: 6            taatttgatggccata 21                            </p> <p>Sbjct: 51843        taatttgatggccata 51828</p>	<p>Human</p>
<p>11 (C Allele)</p>	<p>gi 21913039 gb AC079111.7  Homo sapiens  chromosome 17, clone RP11-367G9, complete  sequence  Length = 163410  Score = 36.2 bits (18), Expect = 0.53  Identities = 18/18 (100%)  Strand = Plus / Minus</p> <p>Query: 4            atcattgttctgactttc 21                            </p> <p>Sbjct: 110475        atcattgttctgactttc 110458</p>	<p>Human</p>
<p>11 (C Allele)</p>	<p>&gt;gi 37719158 gb AC105075.6  Mus musculus  chromosome 1, clone RP23-366P11, complete  sequence  Length = 195511  Score = 34.2 bits (17), Expect = 2.1  Identities = 17/17 (100%)  Strand = Plus / Minus</p> <p>Query: 5            tcattgttctgactttc 21                            </p> <p>Sbjct: 127117        tcattgttctgactttc 127101</p>	<p>House Mouse</p>



11 (T Allele)	gi 6624738 emb AL049553.20 HSJ402N21 Human DNA sequence from clone RP3-402N21 on chromosome 6p21.1-21.31 Contains the MDGA1 gene for MAM domain containing glycosylphosphatidylinositol anchor 1, the gene for a novel protein and four CpG islands, complete sequence Length = 170302 Score = 42.1 bits (21), Expect = 0.009 Identities = 21/21 (100%) Strand = Plus / Minus  Query: 1        gcaatcattgttctgactttt 21       Sbjct: 80929 gcaatcattgttctgactttt 80909	Human
13 (T Allele)	gi 15638795 gb AC092622.2  Homo sapiens BAC clone RP11-254O14 from 2, complete sequence Length = 19531 Score = 32.2 bits (16), Expect = 8.3 Identities = 16/16 (100%) Strand = Plus / Minus  Query: 6        ggccaagaacaggat 21       Sbjct: 9433    ggccaagaacaggat 9418	Human
13 (C Allele)	gi 15209313 emb AL160398.27  Human DNA sequence from clone RP11-15N12 on chromosome 6 Contains the 5' end of the gene for the possible ortholog of R. norvegicus ion transporter protein (NRITP), complete sequence Length = 134995 Score = 32.2 bits (16), Expect = 8.3 Identities = 16/16 (100%) Strand = Plus / Minus  Query: 6        ggccaagaacaggac 21       Sbjct: 94841    ggccaagaacaggac 94826	Human
13 (C Allele)	gi 16944094 emb AL583889.8  Mouse DNA sequence from clone RP23-10K12 on chromosome 15, complete sequence Length = 236344 Score = 32.2 bits (16), Expect = 8.3	House Mouse

	Identities = 16/16 (100%) Strand = Plus / Minus  Query: 6           ggcccaagaacaggac 21         Sbjct: 78958   ggcccaagaacaggac 78943	
15 (A Allele)	gi 16973887 emb AL512626.8  Human DNA sequence from clone RP11-163I12 on chromosome 1 Contains part of the ESRRG gene for estrogen-related receptor gamma, complete sequence Length = 106859 Score = 32.2 bits (16), Expect = 8.3 Identities = 19/20 (95%) Strand = Plus / Minus  Query: 2           ctgacactcgctgaactcaa 21         Sbjct: 17052   ctgacactctctgaactcaa 17033	Human
15 (A Allele)	gi 23820923 gb AC122270.4  Mus musculus BAC clone RP23-220N16 from 17, complete sequence Length = 196395 Score = 30.2 bits (15), Expect = 33 Identities = 15/15 (100%) Strand = Plus / Minus  Query: 7           actcgctgaactcaa 21         Sbjct: 64658   actcgctgaactcaa 64644	House Mouse
15 (A Allele)	gi 62543315 gb AC123544.4  Lemur catta clone LB2-246N5, complete sequence Length = 195323 Score = 30.2 bits (15), Expect = 33 Identities = 18/19 (94%) Strand = Plus / Minus  Query: 3           tgacactcgctgaactcaa 21         Sbjct: 1362   tgacaatcgctgaactcaa 1344	Ring- tailed Lemur
15 (G Allele)	gi 60418190 gb AC108828.17  Mus musculus chromosome 5, clone RP23-153H17, complete sequence Length = 218103 Score = 34.2 bits (17), Expect = 2.1 Identities = 17/17 (100%) Strand = Plus / Minus	House Mouse

	Query: 5           acactcgctgaactcag 21         Sbjct: 146785   acactcgctgaactcag 146769	
15 (G Allele)	gi 22002199 gb AC099787.2  Homo sapiens chromosome 1 clone RP4-538N4, complete sequence Length = 177329 Score = 32.2 bits (16), Expect = 8.3 Identities = 16/16 (100%) Strand = Plus / Plus  Query: 6           cactcgctgaactcag 21         Sbjct: 61135   cactcgctgaactcag 61150	Human
17 (T Allele)	gi 30409940 gb AC123056.4  Mus musculus BAC clone RP23-182H4 from chromosome 13, complete sequence Length = 183076 Score = 36.2 bits (18), Expect = 0.53 Identities = 18/18 (100%) Strand = Plus / Plus  Query: 4           gaaagaccacattatttt 21         Sbjct: 86528   gaaagaccacattatttt 86545	House Mouse
17 (T Allele)	gi 2791551 emb AL008725.1 HS148E22 Human DNA sequence from clone RP1-148E22 on chromosome 20q12-13.12 Contains the YWHAB gene encoding tyrosine 3-monooxygenase/ntryptophan 5- monooxygenase activation protein, beta polypeptide, a novel gene similar to PABPC1 (poly (A)-binding protein, cytoplasmic 1), 2 CpG islands, ESTs, STSs and GSSs, complete sequence Length = 79227 Score = 34.2 bits (17), Expect = 2.1 Identities = 17/17 (100%) Strand = Plus / Minus  Query: 5           aaagaccacattatttt 21         Sbjct: 15937   aaagaccacattatttt 15921	Human
17 (T Allele)	gi 31044300 gb AC129066.3  Didelphis virginiana clone LB3-8N21, complete sequence Length = 158526 Score = 34.2 bits (17), Expect = 2.1	North American Opossum

	Identities = 17/17 (100%) Strand = Plus / Minus  Query: 5           aaagaccacattattttt 21         Sbjct: 52085   aaagaccacattattttt 52069	
17 (T Allele)	gi 29294415 gb AC142296.1  Pan troglodytes BAC clone RP43-97L1 from Y, complete sequence Length = 158231 Score = 32.2 bits (16), Expect = 8.3 Identities = 16/16 (100%) Strand = Plus / Minus  Query: 6           aagaccacattattttt 21         Sbjct: 101310   aagaccacattattttt 101295	Chimpanzee
17 (T Allele)	gi 30270589 gb AC120570.5  Rattus norvegicus 1 BAC CH230-96N8 (Children's Hospital Oakland Research Institute) complete sequence Length = 227607 Score = 32.2 bits (16), Expect = 8.3 Identities = 16/16 (100%) Strand = Plus / Minus  Query: 6           aagaccacattattttt 21         Sbjct: 184656   aagaccacattattttt 184641	Norway Rat
17 (A Allele)	gi 48675476 gb AC144933.4  Mus musculus BAC clone RP24-531B24 from chromosome 8, complete sequence Length = 169667 Score = 36.2 bits (18), Expect = 0.21 Identities = 18/18 (100%) Strand = Plus / Minus  Query: 1           gaaagaccacattatttta 18         Sbjct: 118910   gaaagaccacattatttta 118893	House Mouse
17 (A Allele)	gi 11096675 emb AL356794.10  Human DNA sequence from clone RP11-551A11 on chromosome 6 Contains a ribosomal protein S3A (40S ribosomal protein S3a, v-fos transformation effector protein 1) (RPS3A) (FTE1) pseudogene, complete sequence Length = 164439	Human

	<p>Score = 34.2 bits (17), Expect = 2.1  Identities = 20/21 (95%)  Strand = Plus / Minus</p> <p>Query: 1            tgggaaagaccacattatttta 21       </p> <p>Sbjct: 142830 tgggaaagaccactttatttta  142810</p>	
19 (A Allele)	<p>gi 29823238 emb AL844164.17  Mouse DNA  sequence from clone RP23-300I3 on  chromosome 4, complete  sequence  Length = 209214  Score = 40.1 bits (20), Expect = 0.034  Identities = 20/20 (100%)  Strand = Plus / Minus</p> <p>Query: 2            gtctgaaacaaaagggaaca 21       </p> <p>Sbjct: 24553 gtctgaaacaaaagggaaca 24534</p>	House Mouse
19 (A Allele)	<p>gi 62123257 gb AC159375.1  Pan  troglodytes chromosome UNKNOWN clone  CH251-557H18, complete  sequence  Length = 184511  Score = 34.2 bits (17), Expect = 2.1  Identities = 17/17 (100%)  Strand = Plus / Plus</p> <p>Query: 5            tgaaacaaaagggaaca 21       </p> <p>Sbjct: 42683 tgaaacaaaagggaaca 42699</p>	Chimpanzee
19 (A Allele)	<p>gi 20503261 gb AC115112.5  Homo sapiens  BAC clone RP11-427M12 from 4, complete  sequence  Length = 142494</p> <p>Score = 34.2 bits (17), Expect = 2.1  Identities = 17/17 (100%)  Strand = Plus / Plus</p> <p>Query: 5            tgaaacaaaagggaaca 21       </p> <p>Sbjct: 117698 tgaaacaaaagggaaca 117714</p>	Human
19 (T Allele)	<p>gi 20564428 gb AC073372.9  Homo sapiens  chromosome 11 clone RP11-500D4, complete  sequence  Length = 180504  Score = 38.2 bits (19), Expect = 0.14</p>	Human

	Identities = 19/19 (100%) Strand = Plus / Minus  Query: 3            tctgaaacaaaagggaact 21       Sbjct: 163198      tctgaaacaaaagggaact 163180	
19 (T Allele)	gi 51241710 emb AL808125.11  Mouse DNA sequence from clone RP23-193L22 on chromosome 2, complete sequence Length = 236619 Score = 34.2 bits (17), Expect = 2.1 Identities = 17/17 (100%) Strand = Plus / Plus  Query: 5            tgaaacaaaagggaact 21       Sbjct: 28213      tgaaacaaaagggaact 28229	House Mouse
21 (G Allele)	gi 56787768 gb AC123698.15  Mus musculus chromosome 15, clone RP23-331P14, complete sequence Length = 201739 Score = 32.2 bits (16), Expect = 8.3 Identities = 19/20 (95%) Strand = Plus / Plus  Query: 2            atgagtaagaagcatccggg 21       Sbjct: 150709 atgagcaagaagcatccggg 150728	House Mouse
71 (C Allele)	gi 20339152 emb AL670720.7  Mouse DNA sequence from clone RP23-321M9 on chromosome 4, complete sequence Length = 200628 Score = 32.2 bits (16), Expect = 8.3 Identities = 16/16 (100%) Strand = Plus / Plus  Query: 6            ccagactattgggacc 21       Sbjct: 102456      ccagactattgggacc 102471	House Mouse
45 (C Allele)	gi 18044094 gb BC019461.1  Mus musculus DNA segment, Chr 4, Brigham & Women's Genetics 1540 expressed, mRNA (cDNA clone MGC:28642 IMAGE:4224033), complete cds Length = 1461 Score = 38.2 bits (19), Expect = 0.14	House Mouse

	Identities = 19/19 (100%) Strand = Plus / Plus  Query: 3           gaacggagagcaggccttc 21         Sbjct: 1158       gaacggagagcaggccttc 1176	
45 (G Allele)	gi 28867179 gb AC123925.4  Mus musculus BAC clone RP24-292N2 from chromosome 15, complete sequence Length = 166696 Score = 34.2 bits (17), Expect = 2.1 Identities = 17/17 (100%) Strand = Plus / Plus  Query: 5           acggagagcaggccttg 21         Sbjct: 8541       acggagagcaggccttg 8557	House Mouse
45 (G Allele)	gi 37790797 gb AY436323.1  Homo sapiens angiotensinogen (serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 8) (AGT) gene, complete cds Length = 15593 Score = 32.2 bits (16), Expect = 8.3 Identities = 16/16 (100%) Strand = Plus / Plus  Query: 6           cggagagcaggccttg 21         Sbjct: 7852       cggagagcaggccttg 7867	Human
25 (C Allele)	gi 5649375 gb AC007253.2  Homo sapiens BAC clone RP11-454P5 from 2, complete sequence Length = 225699 Score = 32.2 bits (16), Expect = 8.3 Identities = 16/16 (100%) Strand = Plus / Minus  Query: 6           gaacaggattgagttc 21         Sbjct: 202335     gaacaggattgagttc 202320	Human
25 (C Allele)	gi 62123195 gb AC154832.2  Mus musculus chromosome 14 clone RP24-568D4, complete sequence Length = 134900 Score = 32.2 bits (16), Expect = 8.3 Identities = 19/20 (95%)	House Mouse

	Strand = Plus / Minus  Query: 2        ccaagaacaggattgagttc 21       Sbjct: 1377    ccaaggacaggattgagttc 1358	
25 (T Allele)	gi 62123165 gb AC123530.4  Mus musculus BAC clone RP24-194D2 from chromosome 10, complete sequence Length = 164420 Score = 36.2 bits (18), Expect = 0.53 Identities = 18/18 (100%) Strand = Plus / Plus  Query: 4        aagaacaggattgagttt 21       Sbjct: 52179    aagaacaggattgagttt 52196	House Mouse
25 (T Allele)	gi 51699533 gb AC150516.2  Bos taurus BAC CH240-117L9 (Children's Hospital Oakland Research Institute Bovine BAC Library (male)) complete sequence Length = 237116 Score = 34.2 bits (17), Expect = 2.1 Identities = 17/17 (100%) Strand = Plus / Plus  Query: 2        ccaagaacaggattgag 18       Sbjct: 134113    ccaagaacaggattgag 134129 Score = 26.3 bits (13), Expect = 514 Identities = 13/13 (100%) Strand = Plus / Minus  Query: 9        caggattgagttt 21       Sbjct: 178822    caggattgagttt 178810	Cow
25 (T Allele)	gi 13435286 gb AC019211.6  Homo sapiens BAC clone RP11-454J11 from 2, complete sequence Length = 167471 Score = 32.2 bits (16), Expect = 8.3 Identities = 16/16 (100%) Strand = Plus / Minus  Query: 6        gaacaggattgagttt 21       Sbjct: 48760    gaacaggattgagttt 48745	Human



Clearly, if these sequences are present in horse, they can be and indeed were identified in other species of interest.

Moreover, the amended and new claims are directed to use of SNPs in genetic analysis of genomic DNA obtained from mammals of **the same species**. The application as filed satisfies the written description requirement because it unambiguously conveys to those of skill in the art that the Applicant was in possession of the claimed invention as of the priority date. Applicants' insight that combinations of SNPs would be extremely useful as genetic markers and can be used for genetic analysis follows from their discovery regarding the distribution and density of SNPs in mammalian genomes. While the illustrative examples in the specification are directed to horse and human studies, one of ordinary skill in the art upon reading the specification would readily understand that the methods and use of SNPs would be applicable to all species including mammals. Applicants have described this applicability throughout their specification. This is further demonstrated by the limited BLAST sequence comparison conducted, which identifies the same SNPs that are found in horses are found in humans, chimpanzees, mice, ring-tailed lemurs, rats, cows and opossums. Therefore, it is respectfully submitted that the specification fully complies with the written description requirement for methods of identifying single nucleotide polymorphic sites in the genome of mammals of the same species. Accordingly, Applicants respectfully request withdrawal of this rejection.

**Rejections Under 35 U.S.C. § 112, First Paragraph: Enablement**

The Examiner rejected claims 32-45 under 35 U.S.C. § 112, first paragraph for allegedly failing to comply with the enablement requirement. Applicants respectfully traverse this rejection.

While the Examiner asserts that the specification does present several examples directed to the analysis of equine and human DNA, the Examiner concludes that the six examples do not enable identification of mutations in any or all mammalian species.

Applicants respectfully disagree with this rejection, but have amended claims 32-45 in order to expedite prosecution to include methods for identifying single nucleotide polymorphic sites in the genome of mammals of the same species.

Applicants submit that genomic DNA is genomic DNA regardless of the species and DNA does not chemically vary between species. It follows that the analysis of SNPs should not in any way depend on the source of the nucleic acid molecules. As stated above, Applicants performed a limited sequence search for mammals other than horses using NIH BLAST search for exact matches of some of the sequences described in Table I of the specification: Sequences ID Nos. 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 25, 45, and 71. Exact matches were found for mammals other than horses, for example in humans, chimpanzees, mice, rats, cows, ring-tailed lemurs and opossums. Moreover, Applicants are not claiming individual SNPs, but methods using the combinations of SNPs as useful genetic markers to provide valuable genetic information.

The Examiner's reliance on *Genentech v. Novo Nordisk* ("*Genentech*") as analogous to the present case is misplaced. *Genentech* was decided on strikingly different facts. In *Genentech*, the claims recited a method for making human growth hormone in a fusion protein and cleaving the fusion protein to make the growth hormone. The patentees in *Genentech* tried to rely on the level of skill in the art to enable the claim, but at the time of filing the application it was *not* known in the art how to cleave a fusion protein to make growth hormone, *where the cleaving of the fusion protein was the novel aspect of the claim*. In contrast, the novel aspect of the amended claims does not include claims to individual SNPs, but methods using the combinations of SNPs as useful genetic markers. Thus, *Genentech* sheds no light on any alleged written description or enablement issues with respect to the present claims. *Genentech* is simply inapplicable to the facts of this case.

It is respectfully submitted that the specification fully complies with the enablement requirement for methods of identifying single nucleotide polymorphic sites in the genome of mammals of the same species. Accordingly, Applicants respectfully request withdrawal of this rejection.

**Conclusion**

Reconsideration and allowance are respectfully solicited.

Enclosed is the fee for a three-month extension of time and fee for filing a Request For Continued Examination. No additional fee is believed to be due with respect to the filing of this amendment. If any additional fees are due, or an overpayment has been made, please charge, or credit, our Deposit Account No. 11-0171 for such sum.

If the Examiner has any questions regarding the present application, the Examiner is cordially invited to contact Applicant's attorney at the telephone number provided below.

Respectfully submitted,

A handwritten signature in cursive script, appearing to read "William D. Schmidt", written in black ink.

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